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## RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/09/614,221A

TIME: 13:57:25

Input Set : A:\SeqList.txt

Output Set: N:\CRF3\02262002\I614221A.raw

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MAR 12 2002  
TECH CENTER 1600-2900

```

2 <110> APPLICANT: Karunanandaa, Balasulojini
3 Yu, Jaehyuk
4 Kishore, Ganesh M.
6 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
7 WITH STEROL SYNTHESIS AND METABOLISM
9 <130> FILE REFERENCE: 16516.075
11 <140> CURRENT APPLICATION NUMBER: US 09/614,221A
C--> 12 <141> CURRENT FILING DATE: 2000-07-12
14 <150> PRIOR APPLICATION NUMBER: US 60/142,981
15 <151> PRIOR FILING DATE: 1999-07-12
17 <160> NUMBER OF SEQ ID NOS: 626
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1358
21 <212> TYPE: DNA
22 <213> ORGANISM: Glycine max
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (24)...(1100)
28 <400> SEQUENCE: 1
30 gaattcggct cgagtttgaa cca atg aca atg ctt cag aaa atg gct gag ctt 53
31 Met Thr Met Leu Gln Lys Met Ala Glu Leu
32 1 5 10
34 atg gag tac tct tac ctg tta gat atg gcg gac aag act gag gat cca 101
35 Met Glu Tyr Ser Tyr Leu Leu Asp Met Ala Asp Lys Thr Glu Asp Pro
36 15 20 25
38 tac atg aga cta gta tat gct tca tca ttc ttt ata tct gtc tac tat 149
39 Tyr Met Arg Leu Val Tyr Ala Ser Ser Phe Phe Ile Ser Val Tyr Tyr
40 30 35 40
42 gcc tat caa cga acg tgg aag cca ttc aat cca att ctt ggt gag act 197
43 Ala Tyr Gln Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr
44 45 50 55
46 tat gaa atg gtt aac cat ggt ggc att aca ttt ata tca gag cag gtc 245
47 Tyr Glu Met Val Asn His Gly Gly Ile Thr Phe Ile Ser Glu Gln Val
48 60 65 70
50 agt cat cac cct cca atg agt gct ggg cat gct gaa act gaa cat ttc 293
51 Ser His His Pro Pro Met Ser Ala Gly His Ala Glu Thr Glu His Phe
52 75 80 85 90
54 act tat gat gtt aca tca aaa ttg aaa acc aaa ttt ctc ggc aac tca 341
55 Thr Tyr Asp Val Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser
56 95 100 105
58 gtt gat gta tat cct gtt gga aga acg cgt gtt acc ctc aaa aga gat 389
59 Val Asp Val Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Arg Asp
60 110 115 120

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62 ggt gtg gtc ctt gat ttg gtg cct cct cct aca aaa gtt agc aac ttg      437
63 Gly Val Val Leu Asp Leu Val Pro Pro Pro Thr Lys Val Ser Asn Leu
64      125      130      135
66 att ttt gga cga act tgg att gat tca cca gga gag atg atc ctg aca      485
67 Ile Phe Gly Arg Thr Trp Ile Asp Ser Pro Gly Glu Met Ile Leu Thr
68      140      145      150
70 aat ctg act aca ggg gac aaa gtg gtg ctg tat ttt caa cca tgt ggc      533
71 Asn Leu Thr Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly
72 155      160      165      170
74 tgg ttt gga tat gaa gtg gat ggg tac gtg tat aat tct gct gac gag      581
75 Trp Phe Gly Tyr Glu Val Asp Gly Tyr Val Tyr Asn Ser Ala Asp Glu
76      175      180      185
78 cct aag ata ctg atg act gga aaa tgg aat gag gct atg aat tat caa      629
79 Pro Lys Ile Leu Met Thr Gly Lys Trp Asn Glu Ala Met Asn Tyr Gln
80      190      195      200
82 gtt tgt gac tca gag gga gaa cca ctt cca ggc act gag ttg aaa gag      677
83 Val Cys Asp Ser Glu Gly Glu Pro Leu Pro Gly Thr Glu Leu Lys Glu
84      205      210      215
86 att tgg aga gtt gct gat acc ccg aag aag gac aag ttc cag tac acg      725
87 Ile Trp Arg Val Ala Asp Thr Pro Lys Lys Asp Lys Phe Gln Tyr Thr
88      220      225      230
90 cat ttt gca cac aag att aac agc ttt gac act gct ccc aag aag ttg      773
91 His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala Pro Lys Lys Leu
92 235      240      245      250
94 ttg gca tct gac tct cgt cta cgt cct gat aga atg gcc ctt gag aag      821
95 Leu Ala Ser Asp Ser Arg Leu Arg Pro Asp Arg Met Ala Leu Glu Lys
96      255      260      265
98 ggt gac cta tcc aca tct ggt tat gag aag agc agt ttg gag gag agg      869
99 Gly Asp Leu Ser Thr Ser Gly Tyr Glu Lys Ser Ser Leu Glu Glu Arg
100      270      275      280
102 caa aga gct gag aag aga aac cga gag gcc aag ggc cat aag ttc act      917
103 Gln Arg Ala Glu Lys Arg Asn Arg Glu Ala Lys Gly His Lys Phe Thr
104      285      290      295
106 cct aga tgg ttt gat tta aca gat gaa gta act cct acc cct tgg ggt      965
107 Pro Arg Trp Phe Asp Leu Thr Asp Glu Val Thr Pro Thr Pro Trp Gly
108      300      305      310
110 gac ttg gaa gtt tac caa tac aac ggt aaa tat acc caa cat tgt gct      1013
111 Asp Leu Glu Val Tyr Gln Tyr Asn Gly Lys Tyr Thr Gln His Cys Ala
112 315      320      325      330
114 gcc gtt gat agt tct gag tgc att gaa gtg cct gac atc aga cca gaa      1061
115 Ala Val Asp Ser Ser Glu Cys Ile Glu Val Pro Asp Ile Arg Pro Glu
116      335      340      345
118 ttc aac cct tgg caa tat gat aat ttg gat gct gaa tag tgagcctcct      1110
119 Phe Asn Pro Trp Gln Tyr Asp Asn Leu Asp Ala Glu
120      350      355
122 tgtggaattc tttctatattt ttttaaatat cattttgtta ttaagtttgt aatgtaatct      1170
124 tgattggaat gcttgaaatt tggttttgtt tttgggttgt tttatcactg tagtatttga      1230
126 ttaattaata gtagctatgt tagttcatca gttcactttg catggataaaa tgctagtagg      1290
128 gaaattaaag ttatcttcca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagggc      1350

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Input Set : A:\SeqList.txt

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130 ggacgccg 1358
133 <210> SEQ ID NO: 2
134 <211> LENGTH: 1136
135 <212> TYPE: DNA
136 <213> ORGANISM: Glycine max
138 <220> FEATURE:
139 <221> NAME/KEY: CDS
140 <222> LOCATION: (73)...(975)
142 <400> SEQUENCE: 2
144 gaattcggct cgaggtcaca acttcagtgc tatgggtgaat cagtgtattg cacaggttcg 60
146 gacttgctaa gc atg tgc aac aat ggt cag agt cca ctt gat agg ttc ata 111
147 Met Cys Asn Asn Gly Gln Ser Pro Leu Asp Arg Phe Ile
148 1 5 10
150 tct gtg gta gca tgg tgc ata tct acc act cgc cct gtg act ttt ggt 159
151 Ser Val Val Ala Trp Cys Ile Ser Thr Thr Arg Pro Val Thr Phe Gly
152 15 20 25
154 gtt gct cct tat aat ccc att ctt ggt gag aca cac cat gtt tca agg 207
155 Val Ala Pro Tyr Asn Pro Ile Leu Gly Glu Thr His His Val Ser Arg
156 30 35 40 45
158 gga aat ctt aat gtg tta ttg gag cag att tca cat cac cct cca gta 255
159 Gly Asn Leu Asn Val Leu Leu Glu Gln Ile Ser His His Pro Pro Val
160 50 55 60
162 act gct ctc cat gca aca gat gag aag gaa aac att gaa atg tta tgg 303
163 Thr Ala Leu His Ala Thr Asp Glu Lys Glu Asn Ile Glu Met Leu Trp
164 65 70 75
166 tgc cag cga cct gat cca aag ttt aat ggc aca tca gtt gaa gct aaa 351
167 Cys Gln Arg Pro Asp Pro Lys Phe Asn Gly Thr Ser Val Glu Ala Lys
168 80 85 90
170 gtg cat gga ata cgc cag ttg aag ctc cta aat cat ggt gaa aca tat 399
171 Val His Gly Ile Arg Gln Leu Lys Leu Leu Asn His Gly Glu Thr Tyr
172 95 100 105
174 gaa atg aat tgt cct cgc ctt tta ctt aga att ctt cca gtt cct ggt 447
175 Glu Met Asn Cys Pro Arg Leu Leu Leu Arg Ile Leu Pro Val Pro Gly
176 110 115 120 125
178 gct gat tgg gct ggt aca gtt aat ata cgg tgc cta gag aca ggt cta 495
179 Ala Asp Trp Ala Gly Thr Val Asn Ile Arg Cys Leu Glu Thr Gly Leu
180 130 135 140
182 gta gct gaa tta tcc tac aga tca agt tct ttt cta gga att ggg ggg 543
183 Val Ala Glu Leu Ser Tyr Arg Ser Ser Ser Phe Leu Gly Ile Gly Gly
184 145 150 155
186 aat cat aga gtg atc aaa ggg aag atc ctt gac tct tca tca ttg aaa 591
187 Asn His Arg Val Ile Lys Gly Lys Ile Leu Asp Ser Ser Ser Leu Lys
188 160 165 170
190 gtt cta tat gaa gtt gat ggt cat tgg gat agg acc gta aaa gtg aag 639
191 Val Leu Tyr Glu Val Asp Gly His Trp Asp Arg Thr Val Lys Val Lys
192 175 180 185
194 gac aca aat aat ggg aaa gta aga gtg ata tat gat gca aag gaa gtt 687
195 Asp Thr Asn Asn Gly Lys Val Arg Val Ile Tyr Asp Ala Lys Glu Val
196 190 195 200 205

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DATE: 02/26/2002

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198 atg tca ggt ctc gaa act cct ata ctc aag gac ata gag ggt gtg tgg      735
199 Met Ser Gly Leu Glu Thr Pro Ile Leu Lys Asp Ile Glu Gly Val Trp
200                               210                               215                               220
202 caa aca gaa tca gct cat gtt tgg ggt gaa tta aac caa gcc att gtg      783
203 Gln Thr Glu Ser Ala His Val Trp Gly Glu Leu Asn Gln Ala Ile Val
204                               225                               230                               235
206 agc aaa gac tgg gag aaa gca aga gaa gca aag cta aaa gtt gag gaa      831
207 Ser Lys Asp Trp Glu Lys Ala Arg Glu Ala Lys Leu Lys Val Glu Glu
208                               240                               245                               250
210 aga caa agg gag ctt gtg aga gaa aga gaa tca aaa gga gaa aca tgg      879
211 Arg Gln Arg Glu Leu Val Arg Glu Arg Glu Ser Lys Gly Glu Thr Trp
212                               255                               260                               265
214 att tct aag cat ttt gta gtt tct aac aac aaa gaa ggg tgg caa tgt      927
215 Ile Ser Lys His Phe Val Val Ser Asn Asn Lys Glu Gly Trp Gln Cys
216 270                               275                               280                               285
218 tca cct att cat aag agt gta cct gcg gcc ccc atc aca gcc cta taa      975
219 Ser Pro Ile His Lys Ser Val Pro Ala Ala Pro Ile Thr Ala Leu
220                               290                               295                               300
222 ttgtttgtcac tgtcaagtag tgtaaagcat taaagtacat tttagaagag aatgttcata 1035
224 aaaaaatttta atggttgaaa ttttgacaac aatgaagtat ataacaaaat ttaaaattag 1095
226 ttacaatttt aaaaaaaaaa aaaaaaaaaaag ggcggccgcc g 1136
229 <210> SEQ ID NO: 3
230 <211> LENGTH: 1355
231 <212> TYPE: DNA
232 <213> ORGANISM: Glycine max
234 <220> FEATURE:
235 <221> NAME/KEY: CDS
236 <222> LOCATION: (32)...(1099)
238 <400> SEQUENCE: 3
240 ggaattcggc tcgaggacaa tgcttcagaa a atg gct gag ctt atg gag tac      52
241                               Met Ala Glu Leu Met Glu Tyr
242                               1                               5
244 tct tac ctg tta gat atg gcg gac aag act gag gat cca tac atg aga      100
245 Ser Tyr Leu Leu Asp Met Ala Asp Lys Thr Glu Asp Pro Tyr Met Arg
246                               10                               15                               20
248 cta gta tat gct tca tca ttc ttt ata tct gtc tac tat gcc tat caa      148
249 Leu Val Tyr Ala Ser Ser Phe Phe Ile Ser Val Tyr Tyr Ala Tyr Gln
250                               25                               30                               35
252 cga acg tgg aag cca ttc aat cca att ctt ggt gag act tat gaa atg      196
253 Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr Tyr Glu Met
254 40                               45                               50                               55
256 gtt aac cat ggt ggc att aca ttt ata tca gag cag gtc agt cat cac      244
257 Val Asn His Gly Gly Ile Thr Phe Ile Ser Glu Gln Val Ser His His
258                               60                               65                               70
260 cct cca atg agt gct ggg cat gct gaa act gaa cat ttc act tat gat      292
261 Pro Pro Met Ser Ala Gly His Ala Glu Thr Glu His Phe Thr Tyr Asp
262                               75                               80                               85
264 gtt aca tca aaa ttg aaa acc aaa ttt ctc ggc aac tca gtt gat gta      340
265 Val Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser Val Asp Val

```

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266	90	95	100	
268	tat cct gtt gga aga acg cgt gtt acc ctc aaa aga gat ggt gtg gtc	388		
269	Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Arg Asp Gly Val Val			
270	105 110 115			
272	ctt gat ttg gtg cct cct cct aca aaa gtt agc aac ttg att ttt gga	436		
273	Leu Asp Leu Val Pro Pro Pro Thr Lys Val Ser Asn Leu Ile Phe Gly			
274	120 125 130 135			
276	cga act tgg att gat tca cca gga gag atc ctg aca aat ctg act	484		
277	Arg Thr Trp Ile Asp Ser Pro Gly Glu Met Ile Leu Thr Asn Leu Thr			
278	140 145 150			
280	aca ggg gac aaa gtg gtg ctg tat ttt caa cca tgt ggc tgg ttt gga	532		
281	Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly Trp Phe Gly			
282	155 160 165			
284	gct ggt aga tat gaa gtg gat ggg tac gtg tat aat tct gct gac gag	580		
285	Ala Gly Arg Tyr Glu Val Asp Gly Tyr Val Tyr Asn Ser Ala Asp Glu			
286	170 175 180			
288	cct aag ata ctg atg act gga aaa tgg aat gag gct atg aat tat caa	628		
289	Pro Lys Ile Leu Met Thr Gly Lys Trp Asn Glu Ala Met Asn Tyr Gln			
290	185 190 195			
292	gtt tgt gac tca gag gga gaa cca ctt cca ggc act gag ttg aaa gag	676		
293	Val Cys Asp Ser Glu Gly Glu Pro Leu Pro Gly Thr Glu Leu Lys Glu			
294	200 205 210 215			
296	att tgg aga gtt gct gat acc ccg aag aag gag aag ttc cag tac acg	724		
297	Ile Trp Arg Val Ala Asp Thr Pro Lys Lys Asp Lys Phe Gln Tyr Thr			
298	220 225 230			
300	cat ttt gca cac aag att aac agc ttt gac act gct ccc aag aag ttg	772		
301	His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala Pro Lys Lys Leu			
302	235 240 245			
304	ttg gca tct gac tct cgt cta cgt cct gat aga atg gcc ctt gag aag	820		
305	Leu Ala Ser Asp Ser Arg Leu Arg Pro Asp Arg Met Ala Leu Glu Lys			
306	250 255 260			
308	ggt gac cta tcc aca tct ggt tat gag aag agc agt ttg gag gag agg	868		
309	Gly Asp Leu Ser Thr Ser Gly Tyr Glu Lys Ser Ser Leu Glu Glu Arg			
310	265 270 275			
312	caa aga gct gag aag aga aac cga gag gcc aag ggc cat aag ttc act	916		
313	Gln Arg Ala Glu Lys Arg Asn Arg Glu Ala Lys Gly His Lys Phe Thr			
314	280 285 290 295			
316	cct aga tgg ttt gat tta aca gat gaa gta act cct acc cct tgg ggt	964		
317	Pro Arg Trp Phe Asp Leu Thr Asp Glu Val Thr Pro Thr Pro Trp Gly			
318	300 305 310			
320	gac ttg gaa gtt tac caa tac aac ggt aaa tat acc caa cat tgt gct	1012		
321	Asp Leu Glu Val Tyr Gln Tyr Asn Gly Lys Tyr Thr Gln His Cys Ala			
322	315 320 325			
324	gcc gtt gat agt tct gag tgc att gaa gtg cct gac atc aga cca gaa	1060		
325	Ala Val Asp Ser Ser Glu Cys Ile Glu Val Pro Asp Ile Arg Pro Glu			
326	330 335 340			
328	ttc aac cct tgg caa tat gat aat ttg gat gct gaa tag tgagcatcct	1109		
329	Phe Asn Pro Trp Gln Tyr Asp Asn Leu Asp Ala Glu			
330	345 350 355			

## VERIFICATION SUMMARY

DATE: 02/26/2002

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Input Set : A:\SeqList.txt

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:670 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:674 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:801 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:861 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:863 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:942 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:1013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24  
L:1015 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24  
L:1017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24  
L:1019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24  
L:1036 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:1038 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
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L:1090 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1092 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1094 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
L:1142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29